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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/993,756A

DATE: 01/29/2002

TIME: 10:55:29

Input Set : N:\Crf3\RULE60\09993756A.raw

Output Set: N:\CRF3\01292002\I993756A.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:
 5 (i) APPLICANT: Akerblom, Ingrid E.
 7 (ii) TITLE OF INVENTION: A NOVEL HUMAN LEPTIN RECEPTOR
 8 GENE-RELATED PROTEIN
 10 (iii) NUMBER OF SEQUENCES: 4
 12 (iv) CORRESPONDENCE ADDRESS:
 13 (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
 14 (B) STREET: 3174 Porter Drive
 15 (C) CITY: Palo Alto
 16 (D) STATE: CA
 17 (E) COUNTRY: U.S.
 18 (F) ZIP: 94304
 20 (v) COMPUTER READABLE FORM:
 21 (A) MEDIUM TYPE: Diskette
 22 (B) COMPUTER: IBM Compatible
 23 (C) OPERATING SYSTEM: DOS
 24 (D) SOFTWARE: FastSEQ Version 1.5
 26 (vi) CURRENT APPLICATION DATA:
 C--> 27 (A) APPLICATION NUMBER: US/09/993,756A
 C--> 28 (B) FILING DATE: 05-Nov-2001
 30 (vii) PRIOR APPLICATION DATA:
 32 (A) APPLICATION NUMBER: US/09/212,153
 33 (B) FILING DATE:
 34 (A) APPLICATION NUMBER: US/08/843,370
 35 (B) FILING DATE:
 36 (A) APPLICATION NUMBER: US 08/691,071
 37 (B) FILING DATE: August 1, 1996
 39 (viii) ATTORNEY/AGENT INFORMATION:
 40 (A) NAME: Billings, Lucy J.
 41 (B) REGISTRATION NUMBER: 36,749
 42 (C) REFERENCE/DOCKET NUMBER: PF-0111-1 US
 44 (ix) TELECOMMUNICATION INFORMATION:
 45 (A) TELEPHONE: 415-855-0555
 46 (B) TELEFAX: 415-845-4166
 48 (2) INFORMATION FOR SEQ ID NO: 1:
 50 (i) SEQUENCE CHARACTERISTICS:
 51 (A) LENGTH: 131 amino acids
 52 (B) TYPE: amino acid
 53 (C) STRANDEDNESS: single
 54 (D) TOPOLOGY: linear
 56 (ii) MOLECULE TYPE: peptide
 58 (vii) IMMEDIATE SOURCE:

ENTERED

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59      (A) LIBRARY: HNT2NOT01
60      (B) CLONE: 492703
62      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
64 Met Ala Gly Val Lys Ala Leu Val Ala Leu Ser Phe Ser Gly Ala Ile
65   1           5           10           15
66 Gly Leu Thr Phe Leu Met Leu Gly Cys Ala Leu Glu Asp Tyr Gly Val
67           20           25           30
68 Tyr Trp Pro Leu Phe Val Leu Ile Phe His Gly Ile Ser Pro Ile Pro
69           35           40           45
70 His Phe Ile Ala Lys Arg Val Thr Tyr Asp Ser Asp Ala Thr Ser Ser
71           50           55           60
72 Ala Cys Arg Glu Leu Ala Tyr Phe Phe Thr Thr Gly Ile Val Val Ser
73           65           70           75           80
74 Ala Phe Gly Phe Pro Val Ile Leu Ala Arg Val Ala Val Ile Lys Trp
75           85           90           95
76 Gly Ala Cys Gly Leu Val Leu Ala Gly Asn Ala Val Ile Phe Leu Thr
77           100          105          110
78 Ile Gln Gly Phe Phe Leu Ile Phe Gly Arg Gly Asp Asp Phe Ser Trp
79           115          120          125
80 Glu Gln Trp
81           130
83 (2) INFORMATION FOR SEQ ID NO: 2:
85      (i) SEQUENCE CHARACTERISTICS:
86          (A) LENGTH: 874 base pairs
87          (B) TYPE: nucleic acid
88          (C) STRANDEDNESS: single
89          (D) TOPOLOGY: linear
91      (ii) MOLECULE TYPE: cDNA
93      (vii) IMMEDIATE SOURCE:
94          (A) LIBRARY: HNT2NOT01
95          (B) CLONE: 492703
97      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
99 GTCTGGCTTG GGCAGGCTGC CCGGGCCGTG GCAGGAAGCS GGAAGCAGCC GCGGCCCCAG      60
100 TTCGGGAGAC ATGGCGGGCG TTAAAGCTCT CGTGGCATTG TCCTTCAGTG GGGCTATTGG      120
101 ACTGACTTTT CTTATGCTGG GATGTGCCTT AGAGGATTAT GGCGTTTACT GGCCCTTATT      180
102 CGTCCTGATT TTCCACGGCA TCTCCCCCAT CCCCATTTC ATTGCCAAAA GAGTCACCTA      240
103 TGACTCAGAT GCAACCAGTA GTGCCTGTCG GGAAGTGGCA TATTTCTTCA CTAAGTGAAT      300
104 TGTTGTTTCT GCCTTTGGAT TTCCTGTTAT TCTTGCTCGT GTGGCTGTGA TCAAATGGGG      360
105 AGCCTGCGGC CTTGTGTTGG CAGGCAATGC AGTCATTTTC CTTACAATTC AAGGGTTTTT      420
106 CCTTATATTT GGAAGAGGAG ATGATTTTAG CTGGGAGCAG TGGTAGCACT TTATTCTGAT      480
107 TACAGTGCAT TGAATTTCTT AGAACTCATA CTATCTGTAT ACATGTGCAC ATGCGGCATT      540
108 TTACTATGAA ATTTAATATG CTGGGTTTTT TAATACCTTT ATATATCATG TTCACCTTAA      600
109 GAAAGACTTC ATAAGTAGGA GATGAGTTTT ATTCTCAGCA AATAGACCTG TCAAATTTAG      660
110 ATTATGTTAC TCAAATTATG TTAAGTGTTC GGCTGTTCAT GTAGTCACGG TGCTCTCAGA      720
111 AAATATATTA ACGCAGTCTT GTAGGCAGCT GCCACCTTAT GCAGTGCATC GAAACCTTTT      780
112 GCTTGGGGAT GTGCTTGGAG AGGCAGATAA CGCTGAAGCA GGCCTCTCAT GACCCAGGAA      840
113 GGCCGGGGTG GWTCCCTCTT TKTTTTGTAG TCCA      874
115 (2) INFORMATION FOR SEQ ID NO: 3:
117      (i) SEQUENCE CHARACTERISTICS:

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118      (A) LENGTH: 145 amino acids
119      (B) TYPE: amino acid
120      (C) STRANDEDNESS: single
121      (D) TOPOLOGY: linear
123      (ii) MOLECULE TYPE: peptide
125      (vii) IMMEDIATE SOURCE:
126          (A) LIBRARY: GenBank
127          (B) CLONE: 733888
129      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
131 Met Cys Cys His Ile His Ile Gln Cys Phe Asp Cys Cys Ser Met Lys
132   1             5             10             15
133 Asn Thr Ile Leu Ala Val Ala Ala Leu Ala Phe Ala Gly Val Val Gly
134             20             25             30
135 Leu Thr Phe Leu Val Leu Gly Cys Ala Leu Pro Arg Tyr Gly Thr Trp
136             35             40             45
137 Thr Pro Met Phe Val Ile Thr Phe Tyr Val Leu Ser Pro Val Pro Leu
138             50             55             60
139 Leu Ile Ala Arg Arg Phe Gln Glu Asp Met Thr Gly Thr Asn Ala Cys
140             65             70             75             80
141 Ile Glu Leu Ala Leu Phe Ile Thr Thr Gly Ile Val Ile Ser Ala Phe
142             85             90             95
143 Ala Leu Pro Ile Val Leu Ala His Ala Gly Thr Ile Ala Met Ser Ala
144             100            105            110
145 Cys Phe Leu Ile Phe Ile Ala Asn Ser Ile Asn Phe Ser Val Ile Ile
146             115            120            125
147 Phe Tyr Phe Arg Ile Phe Asn Gly Glu Asp Met Asn Gly Met Ser Leu
148             130            135            140
149 Trp
150 145
152 (2) INFORMATION FOR SEQ ID NO: 4:
154      (i) SEQUENCE CHARACTERISTICS:
155          (A) LENGTH: 140 amino acids
156          (B) TYPE: amino acid
157          (C) STRANDEDNESS: single
158          (D) TOPOLOGY: linear
160      (ii) MOLECULE TYPE: peptide
162      (vii) IMMEDIATE SOURCE:
163          (A) LIBRARY: GenBank
164          (B) CLONE: 1197072
166      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
168 Met Met Glu Phe Lys Val Ser Pro Leu Thr Lys Ile Ile Ser Leu Ser
169   1             5             10             15
170 Gly Phe Leu Ala Leu Gly Phe Leu Leu Val Ile Leu Ser Cys Ala Leu
171             20             25             30
172 Phe His Asn Tyr Tyr Pro Leu Phe Asp Ile Leu Ile Phe Leu Leu Ala
173             35             40             45
174 Pro Ile Pro Asn Thr Ile Phe Asn Ala Gly Asn Lys Tyr His Thr Ser
175             50             55             60
176 Asp Phe Met Ser Asp Ser Ser Asn Thr Gly Gln Asp Leu Ala His Phe

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177	65				70				75					80
178	Leu	Thr	Gly	Met	Leu	Val	Thr	Ser	Gly	Ile	Ala	Leu	Pro	Val
179					85				90					95
180	Tyr	His	Cys	Gln	Leu	Ile	Gly	His	Leu	Ser	Cys	Ile	Met	Cys
181				100					105					110
182	Gly	Gly	Leu	Ile	Ile	Tyr	Ser	Ser	Ile	Val	Ile	Phe	Lys	Trp
183			115				120					125		
184	Lys	Lys	Asp	Phe	Asn	Glu	Asp	Asp	Ser	Leu	Phe	Gly		
185		130					135					140		

VERIFICATION SUMMARY

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L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]